

SEQUENCE LISTING

<110> TOHOKU TECHNO ARCH CO., LTD.

<120> Novel Diabody-type Bispecific Antibody

<130> AB02035-US

<150> JP 2003-038643

<151> 2003-02-17

<160> 30

<170> PatentIn version 3.1

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<211> 33

<212> DNA

<213> Artificial Sequence

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<223> A NcoI-5H back primer

<400> 1

nnnccatggc ccaggtccag ctgcagcagt ctg 33

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<213> Artificial Sequence

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<223> B 5H-EagI forward primer

<400> 2

nnncggccga ggagactgtg agagtgg 28

<210> 3

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> C EcoRV-5L back primer

<400> 3

nnngatatcc taatgaccca atctcc 26

<210> 4
 <211> 29
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 <220>
 <223> D 5L-SacII forward primer

 <400> 4
 nnnccgcggc acgtttgatt tccagcttg 29

<210> 5
 <211> 32
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 <220>
 <223> E NcoI-h5H back primer

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 <220>
 <223> F h5H-EagI forward primer

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 nnnccggccga gctcacggta accagcgta 29

<210> 7
 <211> 23
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 nnngatatcc agatgaccca gag 23

<210> 8
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 nnnccgcggc gcgggtaatc tgc 23

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 <400> 10
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 <210> 12

<211> 36
<212> DNA
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<220>
<223> L h5L-SacII forward primer

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nnnccgcggc gcgtttaatt tccactttgg tgccac 36

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> M h5H-M48I(+)

<400> 13
gcctggaatg gattgtaac atttatc 27

<210> 14
<211> 27
<212> DNA
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<220>
<223> N h5H-M48I(-)

<400> 14
gataaatggt accaatccat tccaggc 27

<210> 15
<211> 21
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<213> Artificial Sequence

<220>
<223> O h5H-A93T(+)

<400> 15
tattactgca cgcgagtgg c 21

<210> 16
<211> 21
<212> DNA

<213> Artificial Sequence

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<223> P h5H-A93T(-)

<400> 16

gccactgcgc gtgcagtaat a 21

<210> 17

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Q h5H-R66KR71V(+)

<400> 17

atttaagaac aaagtgacca tgacggttga taccagca 38

<210> 18

<211> 38

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<223> R h5H-R66KR71V(-)

<400> 18

tgctggtatc aaccgtcatg gtcactttgt tcttaaat 38

<210> 19

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<213> Artificial Sequence

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<223> S h5H-Y27D(+)

<400> 19

gcctcaggcg atacctttac g 21

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<211> 21

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<213> Artificial Sequence

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 <213> Artificial Sequence

 <220>
 <223> U h5H-M69LT73R(+)

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 <210> 22
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 <223> V h5H-M69LT73R(-)

 <400> 22
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 <210> 23
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 <223> W h5H-I75SS76RA78V(+)

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 <223> X h5H-I75SS76RA78V(-)

<400> 24
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<210> 25
 <211> 354
 <212> DNA
 <213> Mouse

<220>
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 <222> (1)..(354)
 <223> 5H

<400> 25
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 Gln Val Gln Leu Gln Gln Ser Gly Ser Glu Met Ala Arg Pro Gly Ala
 1 5 10 15

tca gtg aag ctg ccc tgc aag gct tct ggc gac aca ttc acc agt tac 96
 Ser Val Lys Leu Pro Cys Lys Ala Ser Gly Asp Thr Phe Thr Ser Tyr
 20 25 30

tgg atg cac tgg gtg aag cag agg cat gga cat ggc cct gag tgg atc 144
 Trp Met His Trp Val Lys Gln Arg His Gly His Gly Pro Glu Trp Ile
 35 40 45

gga aat att tat cca ggt agt ggt ggt act aac tac gct gag aag ttc 192
 Gly Asn Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Ala Glu Lys Phe
 50 55 60

aag aac aag gtc act ctg act gta gac agg tcc tcc cgc aca gtc tac 240
 Lys Asn Lys Val Thr Leu Thr Val Asp Arg Ser Ser Arg Thr Val Tyr
 65 70 75 80

atg cac ctc agc agg ctg aca tct gag gac tct gcg gtc tat tat tgt 288
 Met His Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

aca aga tcg ggg ggt ccc tac ttc ttt gac tac tgg ggc caa ggc acc 336
 Thr Arg Ser Gly Gly Pro Tyr Phe Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

act ctc aca gtc tcc tcc 354
 Thr Leu Thr Val Ser Ser
 115

<210> 26

<211> 342
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (1)..(342)
 <223> 5L

<400> 26
 gac att cta atg acc caa tct cca ctc tcc ctg cct gtc agt ctt gga 48
 Asp Ile Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 gat caa gcc tcc atc tct tgc aga tct agt cag aac att gta cat aat 96
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Asn
 20 25 30
 aat gga atc acc tat tta gaa tgg tac ctg caa agg cca ggc cag tct 144
 Asn Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Arg Pro Gly Gln Ser
 35 40 45
 cca aag ctc ctg atc tac aaa gtt tcc gac cga ttt tct ggg gtc cca 192
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser Gly Val Pro
 50 55 60
 gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 agc aga gta gag gct gag gat ctg gga att tat tac tgc ttt caa ggt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Phe Gln Gly
 85 90 95
 tca cat att cct ccc acg ttc gga ggg ggg acc aag ctg gaa atc aaa 336
 Ser His Ile Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 cgt gcg 342
 Arg Ala

<210> 27
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS

<222> (1)..(357)

<223> Chimeric Sequence (hOH)

<400> 27

cag	gtg	caa	ctg	gtg	cag	agc	ggc	ggt	ggc	gtt	gtg	cag	ccg	ggc	cgc	48
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1			5					10						15		

agc	ctg	cgc	ctg	tct	tgc	aaa	gcg	agc	ggc	tat	acc	ttt	acg	cgc	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	
	20						25						30			

acc	atg	cat	tgg	gtg	cgc	cag	gcg	ccg	ggc	aaa	ggt	ctg	gaa	tgg	att	144
Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	
	35					40					45					

ggc	tat	att	aac	ccg	tct	cgc	ggc	tat	acc	aac	tat	aat	cag	aaa	gtg	192
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Val	
	50					55					60					

aaa	gat	cgc	ttt	acc	att	agc	cgc	gat	aac	tct	aaa	aac	acc	gcg	ttt	240
Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Phe	
65				70				75						80		

ctg	cag	atg	gat	agc	ctg	cgc	ccg	gaa	gat	acc	ggc	gtg	tat	ttt	tgc	288
Leu	Gln	Met	Asp	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Gly	Val	Tyr	Phe	Cys	
			85					90						95		

gcg	cgc	tac	tat	gat	gac	cat	tat	agc	ctg	gat	tat	tgg	ggc	cag	ggc	336
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Ser	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	
		100					105					110				

acc	ccg	gtg	acc	gtt	agc	tcg										357
Thr	Pro	Val	Thr	Val	Ser	Ser										
		115														

<210> 28

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(324)

<223> Chimeric Sequence (hOL)

<400> 28

gat	atc	cag	atg	acc	cag	agc	ccg	agc	tct	ctg	agc	gcg	agc	gtg	ggc	48
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	

1	5	10	15	
gat cgc gtg acc att acg tgc agc gcg tct agc tct gtg agc tat atg				96
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met				
	20	25	30	
aac tgg tac cag caa acc cca ggc aaa gcg ccg aaa cgc tgg att tat				144
Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr				
	35	40	45	
gat acc agc aaa ctg gcg agc ggc gtg ccg agc cgc ttt agc ggc tct				192
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser				
	50	55	60	
ggt agc ggc acc gat tat acg ttt acc att agc tct ctg cag ccg gaa				240
Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu				
	65	70	75	80
gat att gcg acc tat tac tgc cag caa tgg agc tct aac ccg ttt acc				288
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr				
	85	90	95	
ttt ggc cag ggt acc aaa ctg cag att acc cgc gcg				324
Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg Ala				
	100	105		
<210>	29			
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<212>	DNA			
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<221>	CDS			
<222>	(1)..(354)			
<223>	Chimeric Sequence (h5H)			
<400>	29			
cag gtg caa ctg gtt cag agc ggc gcg gaa gtg aaa aag ccg ggc gcg				48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala				
	1	5	10	15
tcg gtt aaa gtg agc tgc aaa gcc tca ggc tat acc ttt acg agc tac				96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr				
	20	25	30	
tgg atg cat tgg gtg cgc cag gcc ccg ggt cag ggc ctg gaa tgg atg				144
Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met				
	35	40	45	

ggt aac att tat ccg ggc agc ggt ggc acc aac tat gcg gaa aaa ttt	192
Gly Asn Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Ala Glu Lys Phe	
50 55 60	

aag aac cgc gtg acc atg acg cgt gat acc agc att tcg acg gcc tat	240
Lys Asn Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr	
65 70 75 80	

atg gaa ctg agc cgc ctg cgt agc gat gac acc gcc gtg tat tac tgc	288
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gcg cgc agt ggc ggt ccg tat ttt ttc gat tac tgg ggc cag ggt acg	336
Ala Arg Ser Gly Gly Pro Tyr Phe Phe Asp Tyr Trp Gly Gln Gly Thr	
100 105 110	

ctg gtt acc gtg agc tcg	354
Leu Val Thr Val Ser Ser	
115	

<210> 30
 <211> 342
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (1)..(342)
 <223> Chimeric Sequence (h5L)

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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly	
1 5 10 15	

gaa ccg gcg tcg att agc tgc cgc agc tcg cag aac atc gtg cat aat	96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Asn	
20 25 30	

aac ggc att acc tat ctg gaa tgg tat ctg cag aaa ccg ggc caa agc	144
Asn Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	

ccg cag ctg tta att tat aaa gtg agc gat cgc ttt agc ggc gtg ccg	192
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser Gly Val Pro	
50 55 60	

gat cgc ttt tcg ggc agc ggt agt ggc acc gat ttt acg ctg aaa att	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	

65	70	75	80	
agc cgc gtg gaa gcg gag gat gtt ggc gtg tat tac tgc ttt cag ggc				288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly				
	85	90	95	
agc cat atc ccg cca acc ttt ggc caa ggc acc aaa gtg gaa att aaa				336
Ser His Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys				
	100	105	110	
cgc gcg				342
Arg Ala				